

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 20, 2000, 14:06:02 ; Search time 9.88 Seconds

(without alignments)
507.675 Million cell updates/sec

Title: US-09-373-230-2

Perfect score: 808
Sequence: 1 NFGRLHCTAVIRININDOVL.....KKDENGDKSYMPTLTNLHQS 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	806	99.8	192	1 IL18_MOUSE	P70380 mus musculu
2	736.5	91.2	194	1 IL18_RAT	P97636 rattus norv
3	538	66.6	193	1 IL18_HORSE	Q9xsq7 equus cabal
4	518	64.1	193	1 IL18_HUMAN	Q14116 homo sapien
5	510	63.1	193	1 IL18_CANFA	Q9xsro canis fami
6	509	63.0	192	1 IL18_PIG	Q19073 sus scrofa
7	82.5	10.2	803	1 ION_HAEIN	P43864 haemophilus
8	82	10.1	267	1 IL18_PIG	P26889 sus scrofa
9	79.5	9.8	526	1 ZABA_YEAST	Q00362 saccharomyc
10	79	9.8	266	1 IL18_BOVIN	P09428 bos taurus
11	78	9.7	1196	1 BXCN_CLOBO	P46081 clostridium
12	77	9.5	885	1 UE3A_MOUSE	Q08759 mus musculu
13	76.5	9.5	167	1 Y809_METJA	Q58219 methanococc
14	76.5	9.5	621	1 HTPG_HELPY	P56116 helicobacte
15	76.5	9.5	269	1 YK70_YEAST	P36166 saccharomyc
16	76	9.4	269	1 IL18_MACMU	P48090 macaca mula
17	76	9.4	270	1 IL18_MACNE	P51493 macaca neme
18	75.5	9.3	439	1 IL1A_MOUSE	P01582 mus musculu
19	75.5	9.3	439	1 Y811_METJA	Q58221 methanococc
20	75.5	9.3	695	1 PRC_HAEIN	P45306 haemophilus
21	75	9.3	266	1 IL18_SHEEP	P21621 ovis aries
22	75	9.3	266	1 IL18_MACFA	P79182 macaca fasc
23	75	9.3	624	1 YB33_SCHPO	Q10198 schizosacch
24	74.5	9.2	270	1 IL1A_PIG	P18430 sus scrofa
25	74	9.2	269	1 IL18_HUMAN	P01584 homo sapien
26	74	9.2	1139	1 RBL2_HUMAN	Q08999 homo sapien
27	73.5	9.1	589	1 TRPG_THEMA	Q08654 thermotoga
28	73	9.0	611	1 HBS1_YEAST	P32769 saccharomyc
29	73	9.0	872	1 VP2_ROTPO	P26191 porcine rot
30	72.5	9.0	698	1 YB06_YEAST	P38283 saccharomyc
31	72.5	9.0	1010	1 WNT5_DROME	P28466 drosophila
32	72	8.9	207	1 ATPF_MYCPN	Q50327 mycoplasma
33	72	8.9	266	1 IL18_CEREL	P51745 cervus elap

34	71.5	8.8	279	1 ATND_CAVPO	O60489 cavia porce
35	71.5	8.8	1215	1 ATC6_YEAST	P39986 saccharomyc
36	71	8.8	165	1 HSCB_BUCAP	O51884 buchnera ap
37	71	8.8	541	1 60IM_HAEIN	P44973 haemophilus
38	71	8.8	628	1 MSIN_HUMAN	Q13421 homo sapien
39	71	8.8	1547	1 TOP2_BOMMO	O16140 bombyx mori
40	70.5	8.7	688	1 EFG_MYCPN	P75544 mycoplasma
41	70.5	8.7	781	1 YB68_SCHPO	Q09748 schizosacch
42	70	8.7	270	1 IL1A_FELCA	O46613 felis silve
43	70	8.7	527	1 RAG2_MOUSE	P21784 mus musculu
44	70	8.7	747	1 AMD1_RAT	P10759 rattus norv
45	70	8.7	1381	1 YBE7_YEAST	P34216 saccharomyc

ALIGNMENTS

```
RESULT 1
ID IL18_MOUSE STANDARD; PRT; 192 AA.
AC P70380;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-18 PRECURSOR (IL-18) (INTERFERON-GAMMA INDUCING FACTOR)
DE (IFN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA).
GN IL18 OR IGIF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=LIVER.
RX MEDLINE; 96061009.
RA Okamura H., Tsutui H., Komatsu T., Yutsudo M., Hakura A.,
RA Tanimoto T., Toriogo K., Okura T., Nakada Y., Hattori K.,
RA Akita K., Namba M., Tanabe F., Konishi K., Fukuda S., Kurimoto M.;
RT "Cloning of a new cytokine that induces IFN-gamma production by T
RT cells.";
RL Nature 378:88-91(1995).
RN [2]
RP SEQUENCE OF 1-191 FROM N.A.
RC STRAIN=NOD; TISSUE=PANCREAS;
RX MEDLINE; 97174346.
RA Rothe H., Jenkins N.A., Copeland N.G., Kolb H.;
RT "Active stage of autoimmune diabetes is associated with the
RT expression of a novel cytokine, IGIF, which is located near Id2.";
RL J. Clin. Invest. 99:469-474(1997).
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
CC -----
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CC -----
DR EMBL; D49949; BAA08705.1; -
DR EMBL; U66244; AAB49753.1; -
DR MGD; MGI:107936; IL18.
KW Cytokine.
FT PROPEP 1 35
FT CHAIN 36 192 INTERLEUKIN-18.
FT CONFLICT 183 185 MFT -> IS (IN REF. 2).
SQ SEQUENCE 192 AA; 22135 MW; 8FED938473874D63 CRC64;
```

Query Match 99.8%; Score 806; DB 1; Length 192;

Best Local Similarity 99.4%; Pred. No. 7.1e-67;
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NEGRHCTTAVIRNINDOVLFDKROVFEEDMTDIDQASASEPQTRLIIYMYKDESEVRGLA 60
DB 36 NEGRHCTTAVIRNINDOVLFDKROVFEEDMTDIDQASASEPQTRLIIYMYKDESEVRGLA 95
QY 61 VTLISVSKDSKXSTLSCNKKIISFEEMDPENIDDIQSDLIFFQKRVPGHNKMEFESSLYE 120
DB 96 VTLISVSKDSKXSTLSCNKKIISFEEMDPENIDDIQSDLIFFQKRVPGHNKMEFESSLYE 155
QY 121 HFLACQKEDDAFKLILKKKDENGDKSVMTLTNLHQS 157
DB 156 HFLACQKEDDAFKLILKKKDENGDKSVMTLTNLHQS 192

RESULT 2

IL18_RAT STANDARD; PRT; 194 AA.

AC P97636; P97637; O88749;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-18 PRECURSOR (IL-18) (INTERFERON-GAMMA INDUCING FACTOR)
DE (IFN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA).
GN IL18 OR IGIF.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=ADRENAL GLAND;
RX MEDLINE; 97152963.
RA Conti B., Jahng J.W., Tintl C., Son J.H., Joh T.H.;
RT "Induction of interferon-gamma inducing factor in the adrenal
cortex";
RL J. Biol. Chem. 272:2035-2037(1997).
RN [2]

CC SEQUENCE FROM N.A.
CC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
CC Culhane A.C., Hall M.D., Rothwell N.J., Lusheshi G.N.;
CC "Cloning of rat brain interleukin-18 cDNA";
CC Mol. Psych. 3:362-366(1998).
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.

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CC -----

DR EMBL; U77776; AAC53009.1; -;
DR EMBL; U77777; AAC53010.1; -;
DR EMBL; AJ222813; CAAL1001.1; -;
KW Cytochrome; Alternative splicing.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 194 INTERLEUKIN-18.
FT VARSPLIC 121 139 MISSING (IN ISOFORM ALPHA).
FT CONFLICT 4 5 MS -> IP (IN REF. 2).
FT CONFLICT 48 48 I -> M (IN REF. 2).
SQ SEQUENCE 194 AA; 22303 MW; E2089AD6F1798450 CRC64;

Query Match 91.2%; Score 736.5; DB 1; Length 194;
Best Local Similarity 89.9%; Pred. No. 1.6e-60;
Matches 142; Conservative 10; Mismatches 5; Indels 1; Gaps 1;

QY 1 NEGRHCTTAVIRNINDOVLFDKRO-PVEEDMTDIDQASASEPQTRLIIYMYKDESEVRGL 59
DB 37 NEGRHCTTAVIRNINDOVLFDKRNPPVEEDMDIDRTANESQTRLIIYMYKDESEVRGL 96
QY 60 AVTLISVSKDSKXSTLSCNKKIISFEEMDPENIDDIQSDLIFFQKRVPGHNKMEFESSLYE 119
DB 97 AVTLISVSKDSKXSTLSCNKKIISFEEMDPENIDDIQSDLIFFQKRVPGHNKMEFESSLYE 156
QY 120 GHFLACQKEDDAFKLILKKKDENGDKSVMTLTNLHQS 157
DB 157 GHFLACQKEDDAFKLILKKKDENGDKSVMTLTNLHQS 194

RESULT 3

IL18_HORSE STANDARD; PRT; 193 AA.

AC Q9XSQ7;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-18 PRECURSOR (IL-18) (INTERFERON-GAMMA INDUCING FACTOR)
DE (IFN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA).
GN IL18 OR IGIF.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
RN [1]
RP SEQUENCE FROM N.A.
RA Nicolson L., Penha-Goncalves M.N., Keanle J.L., Logan N.A.,
RA Argyle D.J., Onions D.E.;
RT "Nucleotide sequence of equine interleukin 12 and 18 cDNAs";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE IL-18 FAMILY.

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CC -----

DR EMBL; Y11131; CAA72013.1; -;
KW Cytochrome.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
SQ SEQUENCE 193 AA; 22058 MW; 4D81535E9004ECAC CRC64;

Query Match 66.6%; Score 538; DB 1; Length 193;
Best Local Similarity 68.8%; Pred. No. 2.1e-42;
Matches 106; Conservative 23; Mismatches 23; Indels 2; Gaps 2;

QY 2 NEGRHCTTAVIRNINDOVLFDK-RQVFEEDMTDIDQASASEPQTRLIIYMYKDESEVRGLA 60
DB 38 NEGRHCTTAVIRNINDOVLFDKRNPPVEEDMDIDRTANESQTRLIIYMYKDESEVRGLA 97
QY 61 VTLISVSKDSKXSTLSCNKKIISFEEMDPENIDDIQSDLIFFQKRVPGH-NKMEFESSLYE 119
DB 98 VTLISVSKDSKXSTLSCNKKIISFEEMDPENIDDIQSDLIFFQKRVPGHDKIQFESSLYE 157
QY 120 GHFLACQKEDDAFKLILKKKDENGDKSVMTLTNLHQS 153
DB 158 GHFLACQKEDDAFKLILKKKDENGDKSVMTLTNLHQS 191

RESULT 4
IL18_HUMAN STANDARD; PRT; 193 AA.
ID IL18_HUMAN

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AC Q14116; 075599;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-18 PRECURSOR (IL-18) (INTERFERON-GAMMA INDUCING FACTOR)
DE (IFN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA).
GN IL18 OR IGIF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE; 96247646.
RA Ushio S., Namba M., Okura T., Hattori K., Nukada Y., Akita K.,
RA Tanabe F., Konishi K., Micallief M., Fujii M., Torigoe K., Tanimoto T.,
RA Fukuda S., Ikeda M., Okamura H., Kurimoto M.;
RT "Cloning of the cDNA for human IFN-gamma-inducing factor, expression
RT in Escherichia coli, and studies on the biologic activities of the
RT protein.";
RL J. Immunol. 156:4274-4279(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Yong D., Guixin D., Lihua H., Haitao W.;
RT "Cloning and sequencing of the cDNA for precursor hIL-18.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 2-193 FROM N.A.
RC TISSUE=PERIPHERAL BLOOD;
RA Conti B., Kim S.J., Tinti C., Chun H.S., Joh T.H.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
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CC -----
DR EMBL; D49950; BAA08706.1; -.
DR EMBL; AF077611; AAC27787.1; -.
DR EMBL; U90434; AAB50010.1; -.
DR MIM; 600953; -.
KW Cytokine.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
FT CONFLICT 66 66 F -> L (IN REF. 2).
FT CONFLICT 86 86 S -> R (IN REF. 2).
FT CONFLICT 191 191 N -> S (IN REF. 2).
SQ SEQUENCE 193 AA; 22326 MW; 323C62C203788D55 CRC64;

Query Match 64.1%; Score 518; DB 1; Length 193;
Best Local Similarity 65.6%; Pred. No. 1.4e-40;
Matches 101; Conservative 26; Mismatches 25; Indels 2; Gaps 2;
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RESULT 5
ID IL18_CANPA STANDARD; PRT; 193 AA.
AC Q9XSRO;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-18 PRECURSOR (IL-18) (INTERFERON-GAMMA INDUCING FACTOR)
DE (IFN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA).
GN IL18 OR IGIF.
OS Canis familiaris (dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RN [1]
RP SEQUENCE FROM N.A.
RA Argyle D.J., McGillivray C., Nicolson L., Onions D.E.;
RT "Cloning, sequencing and characterization of canine interleukin-18.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
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CC -----
DR EMBL; Y11133; CAA72015.1; -.
KW Cytokine.
FT PROPEP 1 36 BY SIMILARITY.
FT CHAIN 37 193 INTERLEUKIN-18.
SQ SEQUENCE 193 AA; 22037 MW; 0D973E586F461F25 CRC64;

Query Match 63.1%; Score 510; DB 1; Length 193;
Best Local Similarity 64.9%; Pred. No. 7.4e-40;
Matches 100; Conservative 25; Mismatches 27; Indels 2; Gaps 2;
```

```
QY 2 FGRHCTTAVIRININDVLFVDK-RQPVFEDMTDIDOSASEPQTRLIIYMYKDSVVRGLA 60
DB 38 FGKLEPKLSIIRNLNDQVLFVNEGMPVFEEDMPDSDCTDNAPHTIIFIYMYKDSLTRGLA 97

QY 61 VTLVKDSKXSTLSCKNKTIISFEEDMPDENIDIOSDLIFQKRVPGH-NKMEFESSLYE 119
DB 98 VTLISVKYKTMSTLSCKNKTIISFKMKSPDSINDEGNDIIFQKRSVPGHDKIQFESSLYK 157

QY 120 GHFLACQKEDDAFKLILKKKDENGDKSVMTLTN 153
DB 158 GHFLACKKENDLFLILKDKDENGDKSIMFTVQN 191

RESULT 6
ID IL18_PIG STANDARD; PRT; 192 AA.
AC O19073;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE INTERLEUKIN-18 PRECURSOR (IL-18) (INTERFERON-GAMMA INDUCING FACTOR)
DE (IFN-GAMMA-INDUCING FACTOR) (INTERLEUKIN-1 GAMMA) (IL-1 GAMMA).
GN IL18 OR IGIF.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN [1]
RP SEQUENCE FROM N.A.
```

RA Foss D.L., Murtaugh M.P.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Muneta Y., Mori Y.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: AUGMENTS NATURAL KILLER CELL ACTIVITY IN SPLEEN CELLS
CC AND STIMULATES INTERFERON GAMMA PRODUCTION IN T HELPER TYPE I
CC CELLS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- SIMILARITY: BELONGS TO THE IL-18 FAMILY.
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CC -----
DR EMBL; U68701; AAC18415.1; -.
DR EMBL; AB010003; BAA24135.1; -.
KW Cytokine.
FT PROPEP 1 35 BY SIMILARITY.
FT CHAIN 36 192 INTERLEUKIN-18.
SQ SEQUENCE 192 AA; 22026 MW; 881EA654E221A17A CRC64;

Query Match 63.0%; Score 509; DB 1; Length 192;
Best Local Similarity 64.9%; Pred. No. 9.1e-40;
Matches 100; Conservative 26; Mismatches 26; Indels 2; Gaps 2;

QY 2 FGRHCTTAVIRNINDQVLFVDK-RQVFEDMTDIDQASAPQTRLIITYMKDSEVRLA 60
Db 37 FGLKLEPKLSTIRNLNDQVLFINGHQAVFEDMPDSDCDNAPQTVFIITYMKDSLTRGLA 96

QY 61 VTLGVKDSKXSTLSCKNKIISFEMDPENIDDIQSDLIFFQKRVPGH-NKMEFESSIVE 119
Db 97 VTISVQCKRMSTLSCKNKITLSFKEMSPDNIDEGNDIIFQRSVPGHDKIQFESSLYK 156

QY 120 GHFLACQKEDDAFKLILKKKDKNGDKSVMTLTN 153
Db 157 GYFLACKKENDLFLKILKEKDECGDKSIMFTVQN 190

RESULT 7
LON_HAEIN STANDARD; PRT; 803 AA.
ID LON_HAEIN
AC P43864;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE ATP-DEPENDENT PROTEASE LA (EC 3.4.21.53).
GN LON OR LON-A OR HI0462.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-RD / KW20;
RX MEDLINE; 95350630.
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
RT influenzae Rd.";
RL Science 269:496-512(1995).

CC -!- FUNCTION: DEGRADES SHORT-LIVED REGULATORY AND ABNORMAL PROTEINS
CC IN PRESENCE OF ATP. DEGRADES THE REGULATORY PROTEINS RCSA AND
CC SULA. HYDROLYZES TWO ATPs FOR EACH PEPTIDE BOND CLEAVED IN THE
CC PROTEIN SUBSTRATE (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF LARGE PROTEINS SUCH AS GLOBIN,
CC CASEIN AND DENATURATED SERUM ALBUMIN, IN PRESENCE OF ATP.
CC -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S16; ALSO KNOWN AS THE
CC LON FAMILY OF ATP-DEPENDENT PROTEASES.
CC -----
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CC -----
DR EMBL; U32729; AAC22121.1; -.
DR TIGR; HI0462; -.
DR INTERPRO; IPR001939; -.
DR INTERPRO; IPR001984; -.
DR PFAM; PF00004; AAA; 1.
DR PRINTS; PR00830; ENDOLAPTASE.
DR PROSITE; PS01046; LON_SER; 1.
KW Hydrolyase; Serine protease; ATP-binding.
FT NP_BIND 356 363 ATP (POTENTIAL).
FT ACT_SITE 679 679 BY SIMILARITY.
SQ SEQUENCE 803 AA; 89347 MW; 9E590852611EEA5B CRC64;

Query Match 10.2%; Score 82.5; DB 1; Length 803;
Best Local Similarity 18.9%; Pred. No. 4.3;
Matches 44; Conservative 33; Mismatches 71; Indels 85; Gaps 7;

QY 3 GRHCTTAVIRNIND-QVLFVDK-RQVFEDMTDIDQAS----- 40
Db 30 GRAKSINALEAMNDKQILLVSQREADLEPTPEDLFVGTIANIIQLKLPDPTVKVL 89

QY 41 -EPQRLIITYMKDSE-----VRGLAVTLSVKDSKXSTLSCKNKIISFE 83
Db 90 VEGQNRKAKINSLDEGEKCFSAQITPIETTYGDEKELVYAKSAVSEFENYLTNKKVPTD 149

QY 84 EMDPPENIDDI-----QSDLIFFQK 103
Db 150 ILNALQRIDVDRLADTMAAHLPVSIHKONALELANVOERLEYLLGMESEADILQVER 209

QY 104 RVPGHNKMEFESSLYEGHFLACQKEDDAFKLILKKKDKNGDKSVMTLTN 156
Db 210 RIRGRVKKQMKES-QRNYYL-----NEQIKAIRKEMDGENEDTIDEVEQLHQ 256

RESULT 8
IL1B_PIG STANDARD; PRT; 267 AA.
ID IL1B_PIG
AC P26889;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
GN IL1B.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93314975.
RA Huebner M.J., Lin G., Smith D.M., Murtaugh M.P., Molitor T.W.;
RT "Cloning, sequencing and regulation of an mRNA encoding porcine
RT interleukin-1 beta.";
RL Gene 129:285-289(1993).
CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES


```
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -1- SUBUNIT: MONOMER.
CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
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CC -----
DR EMBL; M86725; AAA02584.1; -.
DR PIR; JN0724; JN0724.
DR HSSP; P01584; IHB.
DR INTERPRO; IPR000975; -.
DR INTERPRO; IPR002348; -.
DR PFAM; PF00340; Interleukin-1; 1.
DR PRINTS; PR00262; IL1HGF.
DR PRINTS; PR00264; INTERLEUKIN1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT PROPEP 1 114 BY SIMILARITY.
FT CHAIN 115 267 INTERLEUKIN-1 BETA.
SQ SEQUENCE 267 AA; 30404 MW; 7F6B92B784D5086F CRC64;

Query Match 10.1%; Score 82; DB 1; Length 267;
Best Local Similarity 26.1%; Pred. No. 1.3;
Matches 23; Conservative 22; Mismatches 31; Indels 12; Gaps 5;

QY 49 YMKDSEVRGLAVTISVKDSKXSLSCKNK-----IISFEEMDP--PENIDDIQSDLIFF 101
DB 160 FVQGDSDNNKIPVTLGIK-GKNLYLSCVMKDNPTLQLEDIDPKRYPKR--DMEKRFVRY 216

QY 102 OKRVPGHNMKEFESSLYEGHFLACOKED 129
DB 217 KTEI--KNRVEFESALYPMWYISTSQAE 242

RESULT 9
ZABA_YEAST 9
ID ZABA_YEAST STANDARD; PRT; 526 AA.
AC Q00362;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PROTEIN PHOSPHATASE PP2A REGULATORY SUBUNIT B (PR55) (CELL DIVISION
DE CONTROL PROTEIN 55).
GN CDC55 OR YGL190C OR G1345.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92017858.
RA Healy A.M., Zolnierowicz S., Stapleton A.E., Goebel M.,
RA Depaoli-Roach A.A., Pringle J.R.;
RT "CDC55, a Saccharomyces cerevisiae gene involved in cellular
RT morphogenesis: identification, characterization, and homology to the
RT B subunit of mammalian type 2A protein phosphatase.";
RL Mol. Cell. Biol. 11:5767-5780(1991).
RN [2]
```

```
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / FY1679;
RX MEDLINE; 97197971.
RA Coglievina M., Klima R., Bertani I., Delneri D., Zaccaria P.,
RA Bruschi C.V.;
RT "Sequencing of a 40.5 kb fragment located on the left arm of
RT chromosome VII from Saccharomyces cerevisiae.";
RL Yeast 13:55-64(1997).
CC -1- FUNCTION: PHOSPHATASE 2A AFFECTS A VARIETY OF BIOLOGICAL PROCESSES
CC IN THE CELL SUCH AS TRANSCRIPTION, CELL CYCLE PROGRESSION AND
CC CELLULAR MORPHOGENESIS, AND PROVIDES AN INITIAL IDENTIFICATION OF
CC CRITICAL SUBSTRATES FOR THIS PHOSPHATASE. THE REGULATORY SUBUNIT
CC MAY DIRECT THE CATALYTIC SUBUNIT TO DISTINCT, ALBEIT OVERLAPPING,
CC SUBSETS OF SUBSTRATES.
CC -1- SUBUNIT: PP2A EXISTS IN SEVERAL TRIMERIC FORMS, ALL OF WHICH
CC CONSIST OF A CORE COMPOSED OF A CATALYTIC SUBUNIT ASSOCIATED WITH
CC A 65 KDA (PR65) (SUBUNIT A) AND A 55 KDA (PR55) (SUBUNIT B)
CC REGULATORY SUBUNIT.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHATASE 2A REGULATORY SUBUNIT B
CC FAMILY.
CC -----
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CC -----
DR EMBL; M72716; AAA34482.1; -.
DR EMBL; 272712; CAA96902.1; -.
DR EMBL; X91837; CAA62954.1; -.
DR EMBL; X91489; CAA62785.1; -.
DR PIR; A41698; A41698.
DR SGD; S0003158; CDC55.
DR INTERPRO; IPR000009; -.
DR PFAM; PF01240; PR55; 1.
DR PRINTS; PR00600; PP2APR55.
DR PROSITE; PS01024; PR55_1; 1.
DR PROSITE; PS01025; PR55_2; 1.
KW Cell cycle.
FT DOMAIN 416 419 POLY-SER.
FT CONFLICT 500 500 I -> N (IN REF. 1).
SQ SEQUENCE 526 AA; 59662 MW; 6DA12C2805FA6A82 CRC64;

Query Match 9.8%; Score 79.5; DB 1; Length 526;
Best Local Similarity 25.0%; Pred. No. 4.9;
Matches 36; Conservative 29; Mismatches 56; Indels 23; Gaps 7;

QY 14 NINDQVL-FVDRQPVFEDMDIDQASASEPQTRLIIYMKDSEVRGLAVTISVKDSKXST 72
DB 213 DIPDQSFNIVDIKPTNMEELTEVITSAEFHPQECNLFMYSSSK-----GTIKLCDMRONS 267

QY 73 LSCNKKIISFEEMDPENIDDIQSDLIFFQKRVPGHNMKEFESSLYEGHFLACQKEDDAF 132
DB 268 L-CDNKTKTFFEYLDPINHN-----PFTETISSISDIKFSPPN---GRYIASRD----- 311

QY 133 KLILKKKDENGDKSVMTLTNLHQ 156
DB 312 YLTVKIWDVNMNKNKPLKTI-NIHE 334

RESULT 10
IL1B_BOVIN 10
ID IL1B_BOVIN STANDARD; PRT; 266 AA.
AC P09428;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-1 BETA PRECURSOR (IL-1 BETA).
GN IL1B.
OS Bos taurus (Bovine).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89016591.
RA Leong S.R., Flaegs G.M., Lawman M., Gray P.W.;
RT "The nucleotide sequence for the cDNA of bovine interleukin-1 beta.";
RL Nucleic Acids Res. 16:9054-9054(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88318652.
RA Maliszewski C.R., Baker P.E., Schoenborn M.A., Davis B.S., Cosman D.,
RA Gillis S., Cerretti D.P.;
RT "Cloning, sequence and expression of bovine interleukin 1 alpha and
RT interleukin 1 beta complementary DNAs.";
RL Mol. Immunol. 25:429-437(1988).
CC -I- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -I- SUBUNIT: MONOMER.
CC -I- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -I- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -I- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
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CC -----
DR EMBL; M35589; AAA30585.1; -.
DR EMBL; X12498; CAA31018.1; -.
DR EMBL; M37211; AAA30584.1; -.
DR PIR; JL0010; ICBO1B.
DR PIR; S01380; S01380.
DR HSSP; P01584; 1H1B.
DR INTERPRO; IPR000975; -.
DR INTERPRO; IPR002348; -.
DR PFAM; PF00340; interleukin-1; 1.
DR PRINTS; PR00262; IL1HGF.
DR PRINTS; PR00264; INTERLEUKIN1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT PROPEP 1 113
FT CHAIN 114 266 INTERLEUKIN-1 BETA.
FT CONFLICT 252 252 A -> G (IN REF. 2).
SQ SEQUENCE 266 AA; 30774 MW; 9D1EF8F575070586 CRC64;

```

Query Match	9.88;	Score 79;	DB 1;	Length 266;
Best Local Similarity	27.5%;	Pred. No. 2.4;		
Matches 33;	Conservative 18;	Mismatches 33;	Indels 36;	Gaps 8;

QY	40	SEPQTRLIIYMKDSEVRG-----LAVTL SVKDSKXSTLSCKNK----	IISFEEMDP--	87
	:	:::	: :	:
	:	:::	: :	:
Db	146	SQEMNREVFECM--SEVOGEERDNKIPVALGIKD-KNLYLSCVKKGGDPTPLQLLEEVDPKV		202
QY	88	-PENIDDIQSDLIFFQKRVPGHNKMEFEESLYE-----GHFLACQKEDD		130
	:	:::	:::	:
	:	:::	:::	:
Db	203	YPKR--NMEKRFVFKYTEI--KNTVEFESVLYPNWYISTSQIEERPVFLGHFRAGODITD		258

RESULT 11

```
BXCN_CLOBO          STANDARD;          PRT;   1196 AA.
ID    BXCN_CLOBO
AC    PA6081;
DT     01-NOV-1995 (Rel. 32, Created)
DT     01-NOV-1995 (Rel. 32, Last sequence update)
DT     01-NOV-1995 (Rel. 32, Last annotation update)
DE    BOTULINUM NEUROTOXIN TYPE C1, NONTOXIC COMPONENT.
OS    Clostridium botulinum.
OC    Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC    Clostridium.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=TYPE C STOCKHOLM / C-ST;
RX      MEDLINE; 92231894.
RA      Tsuzuki K., Kimura K., Fujii N., Yokosawa N., Oguma K.;
RT      "The complete nucleotide sequence of the gene coding for the
RT      nontoxic-nonhemagglutinin component of Clostridium botulinum type C
RT      progenitor toxin.";
RL      Biochem. Biophys. Res. Commun. 183:1273-1279(1992).
CC      -I- FUNCTION: THE NONTOXIC COMPONENT IS NECESSARY TO MAINTAIN
CC      TOXICITY.
-----
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-----
CC      -----
DR      EMBL: X62389; CAA44262.1; -.
DR      INTERPRO: IPR000395; -.
DR      Pfam: PF01742; Peptidase_M27; 1.
DR      PRINTS: PR00760; BONTOXILYSIN.
KW      Neurotoxin.
SQ      SEQUENCE       1196 AA;  138740 MW;  4BD5956274D7F9C3 CRC64;

Query Match                      9.7%; Score 78; DB 1; Length 1196;
Best Local Similarity           24.3%; Pred. No. 18;
Matches        35; Conservative 23; Mismatches       58; Indels    28; Gaps    4;
```

RESULT	12
UE3A_MOUSE	
ID	UE3A_MOUSE
AC	008759; P97482;
DT	30-MAY-2000 (Rel. 39, Created)
DT	30-MAY-2000 (Rel. 39, Last sequence update)
DT	01-OCT-2000 (Rel. 40, Last annotation update)
DE	UBIQUITIN-PROTEIN LIGASE E3A (EC 6.3.2.-) (ONCOGENIC PROTEIN-ASSOCIATED PROTEIN E6-AP).
GN	UBE3A.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN-C57BL/6 X CBA;
RX	MEDLINE; 97326076.
RA	Hatakeyama S., Jensen J.P., Weissman A.M.;

RT "Subcellular localization and ubiquitin-conjugating enzyme (E2)
 RT interactions of mammalian HECT family ubiquitin protein ligases.";
 RL J. Biol. Chem. 272:15085-15092(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=BRAIN;
 RX MEDLINE: 97264343
 RA Sutcliffe J.S., Jiang Y.-H., Galjaard R.-J., Matsuura T., Fang P.,
 RA Kubota T., Christian S.L., Bressler J., Cattaneach B., Ledbetter D.H.,
 RA Beaudet A.L.;
 RT "The E6-Ap ubiquitin-protein ligase (UBE3A) gene is localized within
 RT a narrowed Angelman syndrome critical region.";
 RL Genome Res. 7:368-377(1997).
 CC -1- FUNCTION: E3 UBIQUITIN-PROTEIN LIGASE WHICH ACCEPTS UBIQUITIN FROM
 CC AN E2 UBIQUITIN-CONJUGATING ENZYME IN THE FORM OF A THIOESTER AND
 CC THEN DIRECTLY TRANSFERS THE UBIQUITIN TO TARGETED SUBSTRATES.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC.
 CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN BRAIN, HEART AND THYMUS.
 CC -1- MISCELLANEOUS: A CYSTEINE RESIDUE IS REQUIRED FOR UBIQUITIN-
 CC THIOLESTER FORMATION.
 CC -1- SIMILARITY: CONTAINS 1 HECT-TYPE E3 UBIQUITIN-PROTEIN LIGASE
 CC DOMAIN.
 CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-38 IS THE INITIATOR.
 CC
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 CC
 CC -----
 CC EMBL: U96636; AAB63361.1; -
 CC EMBL: U82122; AAB47756.1; -
 CC GMD: MGI:105098; UBE3A.
 CC DR INTERPRO: IPR000569; -
 CC DR INTERPRO: IPR002106; -
 CC PFAM: PF00632; HECT; 1.
 CC DR PROSITE: PS50237; HECT; 1.
 CC
 CC KW Nuclear protein; ubiquitin conjugation; ligase.
 CC FT DOMAIN 405 410 ASP/GLU-RICH (ACIDIC).
 CC FT BINDING 786 885 HECT.
 CC FT BINDING 853 853 UBIQUITIN (BY SIMILARITY).
 CC FT CONFLICT 187 187 D -> E (IN REF. 2).
 CC FT CONFLICT 301 301 L -> V (IN REF. 2).
 CC FT CONFLICT 343 343 T -> S (IN REF. 2).
 CC FT CONFLICT 384 384 N -> K (IN REF. 2).
 CC FT CONFLICT 460 460 S -> F (IN REF. 2).
 CC FT CONFLICT 486 486 G -> F (IN REF. 2).
 CC FT CONFLICT 535 535 T -> R (IN REF. 2).
 CC FT CONFLICT 577 577 DEGVVS -> MREAAP (IN REF. 2).
 CC FT CONFLICT 584 584 E -> S (IN REF. 2).
 CC FT CONFLICT 587 587 QL -> SW (IN REF. 2).
 CC FT CONFLICT 597 597 D -> N (IN REF. 2).
 CC FT CONFLICT 623 627 FTLLG -> VYSDWH (IN REF. 2).
 CC FT CONFLICT 725 726 IS -> NL (IN REF. 2).
 CC FT CONFLICT 817 817 L -> Q (IN REF. 2).
 CC FT CONFLICT 869 870 NV -> KE (IN REF. 2).
 CC SQ SEQUENCE 885 AA; 101175 MW; 55D85E080CCB699 CRC64;

Query Match 9.5%; Score 77; DB 1; Length 885;
 Best Local Similarity 26.7%; Pred. No. 15;
 Matches 31; Conservative 20; Mismatches 35; Indels 30; Gaps 7;

QY 14 NINDQVLEVDKROPVE--DMTDIDGASSEPQTRLITYMYKDSVYRGLAVTLVSKDSKXS 71
 DB 402 NHNE---DDEEPIPESELTLQELLDGDERNK-----KGPVDPLETELGVK----- 446

QY 72 TLSCNKIISFEEM--DPENIDDIQSDLIFFQKRVPGHNKMEFESSLYEGHFLAC 125
 DB 447 TLDCRKLISFEESINEPLNDVLEMDKDYTF-----KVETEN--KGSFMTG 491

RESULT 13
 Y809_METJA
 ID Y809_METJA STANDARD; PRT; 167 AA.
 AC Q58219;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HYPOTHETICAL PROTEIN MJ0809.
 GN MJ0809.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
 OC Methanococcus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE: 96337999.
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
 RA jannaschii.";
 RL Science 273:1058-1073(1996).
 CC -1- SIMILARITY: BELONGS TO THE M.JANNASCHII MJ0553 / MJ0809 / MJ1331 /
 CC MJ1405 FAMILY.
 CC
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 CC
 CC -----
 CC EMBL: U67525; AAB98817.1; -
 CC DR TIGR: MJ0809; -
 CC KW Hypothetical protein.
 CC SQ SEQUENCE 167 AA; 19723 MW; DD998FE1329C0042 CRC64;

Query Match 9.5%; Score 76.5; DB 1; Length 167;
 Best Local Similarity 26.8%; Pred. No. 2.3;
 Matches 33; Conservative 16; Mismatches 39; Indels 35; Gaps 5;

QY 47 ILYMYKDSVYRGLAVTLVSKDSK-----XSTLSCKNKIISFEEMDP-----PENID 92
 DB 38 ILYMYKDSVYRGLAVTLVSKDSK-----XSTLSCKNKIISFEEMDP-----PENID 92

QY 93 DIQSDLIFFQKRVPGHNKMEFESSLYEGHFLACQKEDDAFKLLKKKDENGDKSYMFTLT 152
 DB 98 RLSSDDI-----LELNKKLDEG-----VKYIKLIFAELAEH--KKVLEIK 136

QY 153 NLH 155
 DB 137 DMH 139

RESULT 14
 HTPG_HELPY
 ID HTPG_HELPY STANDARD; PRT; 621 AA.
 AC P56116;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HEAT SHOCK PROTEIN HTPG (HIGH TEMPERATURE PROTEIN G).
 GN HTPG OR HP0210.
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;

```
OC Helicobacter.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE: 97394467.
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Wathey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RL pylori."
CC Nature 388:539-547(1997).
CC -i- FUNCTION: MOLECULAR CHAPERONE. HAS ATPASE ACTIVITY
CC (BY SIMILARITY).
CC -i- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 90 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AE000541; AAD07278.1; -.
DR HSSP: P07900; 1YES.
DR TIGR: HP0210; -.
DR INTERPRO: IPR001404; -.
DR PFAM: PF00183; HSP90; 1.
DR PRINTS: PR00775; HEATSHOCK90.
DR PROSITE: PS00298; HSP90; 1.
KW Chaperone; ATP-binding; Heat shock.
SQ SEQUENCE 621 AA; 71274 MW; 28F198C1DC7EAB9A CRC64;

Query Match 9.5%; Score 76.5; DB 1; Length 621;
Best Local Similarity 23.2%; Pred. No. 11;
Matches 29; Conservative 27; Mismatches 52; Indels 17; Gaps 4;

QY 32 MTDIDQASSEPQTRLIYWKDSEVRGLAVTLYSK---DSKXSTLSCKNKIISFEEMDP 88
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 31 LRELVSNASDALDKLNYMLTDEKLGKLTNTPTSIHLSFDSQKTLTIKDNIGMDKNDLI 90

QY 89 ENIDDI-QSDLIFFQKRVPGHNKM-----EFESLSYEGHFLACQKEDDAFKLKKDE 141
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 91 EHLGTIAKSGTKNFTLSALSGDKKDSALIGQGVGYSAFMVAS-----KIVQTKKV 143

QY 142 NGDKS 146
   | | : :
DB 144 NSDQA 148

RESULT 15
YK70_YEAST
ID YK70_YEAST STANDARD; PRT; 706 AA.
AC P36166;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE HYPOTHETICAL 79.4 KDA PROTEIN IN PRP16-SRP40 INTERGENIC REGION.
GN YKR090W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
RN [1]
RP SEQUENCE FROM N.A.
RA Baladron V., Ballesta J.P.G., Bou G., del Rey F., Esteban P.F.,
RA Garcia-Cantalejo J.M., Garcia-Ramirez J.J., Gonzalez A., Jimenez A.,
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RA Revuelta J.L., Santos M.A.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
CC -i- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
CC IONS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: Z28315; CAA82169.1; -.
DR PIR: S38168; S38168.
DR SGD: S0001798; YKR090W.
DR INTERPRO: IPR001781; -.
DR PFAM: PF00412; LIM; 2.
DR PROSITE: PS00478; LIM_DOMAIN_1; 2.
DR PROSITE: PS50023; LIM_DOMAIN_2; 2.
KW Hypothetical protein; LIM motif; Metal-binding; Zinc.
FT DOMAIN 556 612 LIM.
FT DOMAIN 621 672 LIM.
SQ SEQUENCE 706 AA; 79447 MW; B27DB9E09A39AA42 CRC64;

Query Match 9.5%; Score 76.5; DB 1; Length 706;
Best Local Similarity 22.2%; Pred. No. 13;
Matches 35; Conservative 25; Mismatches 63; Indels 35; Gaps 6;

QY 9 TAVIRINDQVLFVDKRPVEEDMTDIDQASSEPQT---RLIYWKDSEVRGLAVTLYS 64
   | : : : | : : | : | : | : | : | : | : | : | : | : | : | :
DB 428 TSIVQNSNTNL---SRQTLVDKGDVDEDAPSESTNGTPIFYKFKQSNVE-----YS 478

QY 65 VKDSKXSTLSCKNKIISFE--EMDPENIDDIQSDLIFFQKRVPGH----- 108
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 479 NNEGMSQETFRTKLPTIEALQDQHKRNITDLREE-IDNSKSNDSHVLPNGGTRYSSDA 537

QY 109 -----NKMFEESLSYEGHFLACQKEDDAFKLKKKDE 141
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 538 DYKETEPIEFKYPPEGPCACGLEVTGKRMFSSKKE 575
```

Search completed: November 20, 2000, 14:07:54
Job time: 112 sec